

FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATC**ATG**CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTTCATGGAGACTACAGCTTTTCGAGGCTACCAAGGCCCTGGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG
AAACTAAG**TAA**ATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG
AACCCTGAAGTTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG
TGTTGAGCTTAGCCTTTGACCTTTCCCTTTTGATCCACAAAATACATTAAACTCTGAATTC
ACATACAATGCTATTTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHA VLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGFLLFETK

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGC**ATG**GCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT
GGGCCTGGCCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTTC
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACC
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC
ACTCTGAGATATATAACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTTCCTGCTTGCA**TAA**CTGATCATATTGCTTGTCTC
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT
TCTATACATAAAAGTTCCTACTTGTTAAA

FIGURE 4

MAVKLGTLALLLALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLWWNGSEPLW
VTLTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHHYGPASPQRKDALKAVDITVLKYMTKWIQERGLQDRNLNVIIFSDHGMDIFW
MDKVIELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFFVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCC
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG
TGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCT
GCGTGCTGCCCCGTTCAGTGTGAACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCCAACACT
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

40261604364

FIGURE 6

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKL
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

[illegible][illegible]

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MLGTTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP
LVTKMCHIGCPDIPSLGLGPYVSIACCQTS LCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCT
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG
CTGGGCTCGGGCGGGGAGTAGGGCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC
GCGGGCTGCGCCCTGGGCAGAGGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCGCCGCGTGGTCAAGCGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA
CAAAATGGCCTACTTCCATGAAGTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTCTGATGGTGATTCTTGATAGG
GCTTTGGAGGAATGGAGATGGGCAAAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTG
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG
TGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA
ATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT
GTGTTTGTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA
GAAAGTGGCATGGAAGTATAAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCTGGATC
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA
GATGAAGTGAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTT
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC
CCAACTTCAAATTCAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA
GTGTTTGATAAAAAATGAAGTGTCTAATATTTATTTTATGGCATCTCATTTTTCAATACAT
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG
TACCATAGAAAAAGTTTGTCTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTC
AAACATTTTACTTAGAGGCAAGGATTTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA
TTATTTTGTAGCTTAAATTAACAGATTTTGTAAATATGTAAGTGTGTTAATAGGTGCATAA
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCCTAAACAAAGATGGTTGTTGCGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC
ATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTGGAACCCATCAGTGATCG
CATATTCATTGATGAGGGTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC
TAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAAGTCTCTGGTCTTCA
TATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRRVSVSGQKVCFAFDKHPCKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNHYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSPNQSTLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCTCAACGTCTATAGCCCCAGCTGAGGTCCCCGAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGGTCATCACCACCCAGGGATCATCGACTCTCACCCTTGGCCCCTAGCTCAGA
AAATCGCAAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCCTTGTATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGGTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCACTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCAGGAATTTCATGGGTGACGTATTCATCAATGTTCCACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCGACCCAGTTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGTCTTTGTGTTCCGAGGTCCCTTCTCA
TGGACGAGAGCTCCCGCTGGCCTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCACCAGGCGG
AACAATATCTGGAGATCAACCCAGTGCCACGGGCCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG
AGACGCTCCCCAGCAAGATACAACAGTGGCACCAGAAGCAGAAGAAGGCCAGGAGGACCTCTGAGGCC
AGGCTGAACCTTCTTGGCTGGGGCAAAACCACTCTCAAGTGGTGGCAGAGTCCAGCACGGCAGCCCGCCTCTC
CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCAACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCCTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTACCCACACCAGGATCGGGTGGGA
CCTGGAGCTAGGGGTGTTTGTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCGAC
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG
CCAGTCCCAGCCCCAGTGCCGGGTCTCCTCCCTTCTGGCTTGGGGAGACAGTTTCTGGGGAGCTTCCAAG
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTCCGGCTATTGTCACA
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAGAGGTTTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCGCCTCTGCCTGGGCTCCCACTTTGCA
GCACTTGAGGAGCCCTTCAACCCGCCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT
CCCTCAGCTTGGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCTTAGCTGCCTCCCCGCGGGGAGGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCTCCCCCAACCCCGTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAG
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCAAGGGCTGAGGAGTGGGGTGCACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTGTGTGAATGCACCAATCCACACTCTGTATCTGGCT
ACTCTGGTGGGGAAGTTGGAGAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAAACAGACCACTTGACTCTCTGTAAAT
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCCCTCCACGCCGTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVGRQVGVKGTDRLVNVFLG
IPFAQPPLGPDREFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIIISGLVLSPVAAGLF
HRAITQSGVITTPGIIIDSHWPPLAQKIANLTLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLA
ISTPVLTSLDVPPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQQKQNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAA
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCT
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACCTCAGCGTG
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATC
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
AGGATCTATGAGAAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG
GTCTCATTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGC GTTCTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCA
ATGAAGGATTTTTTTTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTA ACTACT
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTTCTTTTAAAGTACAGGTTCTTAGTGTTTT
ACTATAACTGTCATATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAA

><MW: 23909, pI: 9.68, NX(S/T): 0

Signal peptide:

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTCGCCTGGCCCTCGCCATGAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCCGCCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC
TATCCCGTGTGTGTTGGGAGCGGGCCCGACGCTGACCCCGCAGAAAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCAGC
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGGATGAAG
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTTCCAACGCCTTCAACCCGGTGTGCGCAACTACAGCATAGACACCCCTGCAGCCCGTGGAGACAACATCAGC
GGTATGGCCCGTGCCTGTACGACCCCAAGCACGCATATGTTGCCCTCTTCTCTGACGGGATGCTCTTACAGCT
ACTGTTACCGACTTCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCTGCGCACCGTG
AAACATGACTCCAAGTGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCCGAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGCTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGGCGTGGTCAGCCTCGGGGGCGGGCCGTG
GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCCGTGGCGAGGATCAG
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCTGATGAGGCACACAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGCGCCCTGGGGCAACAGACCGTT
GTCTTCTGGGTCTGAGGCGGGGACGGTCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGGCCCCGGCGGTGGCGAGACA
GGGAGCGGCTGTGAGCTTGGAGCTGGACGCAGCTTCCGGGGGCGCTGCTGGCTGCCCTTCCCCCGCTGCGTGGT
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAAGACCCCTACTGC
GGGTGGGCCCCGACGGCTCCTGCATCTTCTCAGCCCCGGGCACAGAGCCGCTTTGAGCAGGACGTGTCCGG
GTCAGACCTCAGGCTTAGGGGACTGCACAGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGT
TCGGTGAACCTGCTGGTAACGTGCTGCGTGGCGGCCCTTCTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGG
TGGTTCTGTTGGCCCTCCGTGAGCGGGCGGAGCTGGCCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGC
GGCGAGGCGGTGTGAGCGTCAAGCCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCGGGGCGGAGGCGGT
GGCGGTGGCGCCGGGGTTCCCCCGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
GTGACAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCCCACGCCCCGAGCAGACGCCCTGCCGAGAAGCGC
CTGCCCCACTCCGACCCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCCCGGGCCCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC
CCCCAGCGCCGCTCTATGCTGCCCGGCCCGGCCGCGCCTCCACGGCGACTTCCCGCTCACCCCCCACGCCAGC
CCGACCGCCCGGGGGTGGTGTCCGCGCCCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG
CCCTGGAGCCCGCCCCGACGGGCGAGCTGAGGAGGCCACTGGGCCCCACGCCCCCTCCGGCCGCCACCCTGCGC
CGCACCCACAGTTCAACAGCGCGAGGCCCCGGCCTGGGGACCGCCACCGCGGCTGCCACGCCCCGGCCGGGCACA
GACTTGGCCACCTCCTCCCTATGGGGGGCGGACAGGACTGCGCCCCCGTGGCTAGGCCGGGGGCCCCCG
ATGCCTTGGCAGTGCCAGCCACGGGAACAGGAGCGAGAGACGGTGCCAGAACGCCGGGGCCCCGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCCCCGCGACCCACCCCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACACCAG
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGCTTTGGGGTGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTTGGTTTTTTTTCAGTTTTTGGTTTTCTTTGCGGTTTTCTAAC
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
TGCGTGTGCGTGCCGTGTTCGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGCAGGCTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC
CCCCCCTCTGAGAGGGAAGCGGGACAATGCCGGGTTTCAGGCAGGAGACACGAGGAGGGCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGCTTGGGGCCTGGGGGGCGGCAAGGTGGGTGGGGCCCCCTCTGTAA
ATACGGCCCCAGGGTGGTGAAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGCCCCCTCCCCATCAAT
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1036160-43364

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA
DDLNIQRLVRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG
ECRNFKVLLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSHVYFFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCVSPGDSHFYFNVLQAVTG
VVS LGGRPVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFVLPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGGETGQ
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG
TRAAFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGGPGGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLPA
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPDRRRRVVSAPTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHL LLYGGADRTAPPVP

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCC
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC
CGAAAAGATGGGTCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAGGGCCGGTTT
ACCATGAGAACTGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGAT
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG
GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTCCCTG
GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCATTTTTTGATTTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCATCTACTATGAACATTTTTTACAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAACT
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC
TGAGGACGACCTCTTCCCTTGTAATGTCATAGGAAAAAGACCAAAGATGAACTCTGATATG
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT
TTTTTAAGTATTAATTCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA
TAAAACCACCTTTATTTTAAAGGAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF
TSSPGKEKVFQVKVSAPEEQFTRVGVQVLDKDGSEFIVRYRMYASYKNLKVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLDGWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYFVKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACTTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTAAATTAATTCCTCCAAAGCATTTCGTTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCAAT**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGGGAACT
GGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT
CCCCTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG
TGTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAGCT
AGGTTCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGCGGA
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCACCCCAACCCTGCACAGCCCTCATC
CCCTCTTGGCTTGAAGCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC
CCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP
PLFSKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVS
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDHIGHISGPN SPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

1003601094007

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGAC
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCTTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFESVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
GAAAGGACAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT
CCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGAGCTGGCTGCAAGGGGAACCAG
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT
CAAATTTTAATGGATGATCCCTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT
TAACCCTCACAGCGCTGGATGGTGGGCTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGCTCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGGTTCTTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG
GAGTCAACGCGGAAGTATCCTATTCTTTTTTGTATGCCTCAGAAAATATTTCGAACGACCTTT
CAAATCAATCCTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTT
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTCCAAC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT
CTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAAT
AACGGTCTGGTCTCCGACGTCAATGACAACGCCCCGCGCTTCACCCAAACCTCCTACACCC
TGTTCTGTCGCGAGAACAACAGCCCCGCGCTGCACATCGGCAGCGTCAGCGCCACAGACAGA
GACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCAAGACCCGCACCTGCC
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTGCTGG
ACTACGAGGCCCTGCAGGCTTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCG
CTGAGCAGAGAGGCGCTGGTGCCTGCTGGTGGTGGACGCCAACGACAACCTCGCCCTTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAAATGGGGA
GGTGCACACCGCCAGGCTGCTGAGCGAGCGGACGCGAGCCAAGCACAGGCTCGTGGTGTG
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC
GGCTTCTCCAGCCCTACCTGCCTCTCCCGAGGCGGGCCCCGGCCAGGCCCAGGCCCAGGCG
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTCTCT
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG
TGCTCGGTGCCCCGAGGGTCCTTTTTCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT
GTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT
TCTTGAAACCAGTTATTTTCGGATATTTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT
TCCACCTTCCGAAATAGCTTTGGATTAAATATTTCAGTAAAGTCTGTTTTTAGTTTCATATAC
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTTAAATCTCAAATTTAAGTTAT
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT
TTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTTCTAAATGATAGTGTT
AAGGTTTTAATCTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT
CTGAGGTTTTGATTCAATTCAGAGCTTGCACTCTCATGATTCTAATCACTTCTGTCTATAGTG
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATT
CGTGTGTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTTGGCCAATATTTT
CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAAMGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGKMVCYIQENLPFLLKPSVENFYILITEGALDREIRAENITITVTDLGTPLRKTE
HNITVLVSDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSTNAQVTYSLLPPQDP
HLPLASLVSNADNGHLFALRSLDYEAQAFEFVRGATDRGSPALSREALVRVLVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAAQ
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 25

GAATGAATACCTCCGAAGCCGCTTTGTTCTCCAGATGTGAATAGCTCCACTATACCAGCCTC
GTCTTCCTTCCGGGGGACAACGTGGGTGAGGGCACAGAGAGATATTTAATGTCACCCCTCTTG
GGGCTTTCATGGGACTCCCTCTGCCACATTTTTTGGAGGTTGGGAAAGTTGCTAGAGGCTTC
AGAACTCCAGCCTA**ATG**GATCCCAAACCTCGGGAGAATGGCTGCGTCCCTGCTGGCTGTGCTG
CTGCTGCTGCTGGAGCGCGGCATGTTCTCCTCACCCCTCCCCGCCCCGGCGCTGTTAGAGAA
AGTCTTCCAGTACATTGACCTCCATCAGGATGAATTTGTGCAGACGCTGAAGGAGTGGGTGG
CCATCGAGAGCGACTCTGTCCAGCCTGTGCCTCGCTTCAGACAAGAGCTCTTCAGAATGATG
GCCGTGGCTGCGGACACGCTGCAGCGCCTGGGGGCCCGTGTGGCCTCGGTGGACATGGGTCC
TCAGCAGCTGCCCGATGGTCAGAGTCTTCCAATAACCTCCCGTCATCCTGGCCGAACCTGGGGA
GCGATCCACGAAAGGCACCGTGTGCTTCTACGGCCACTTGGACGTGCAGCCTGCTGACCGG
GGCGATGGGTGGCTCACGGACCCCTATGTGCTGACGGAGGTAGACGGGAAACTTTATGGACG
AGGAGCGACCGACAACAAAGGCCCTGTCTTGGCTTGGATCAATGCTGTGAGCGCCTTCAGAG
CCCTGGAGCAAGATCTTCTGTGAATATCAAATTCATCATTGAGGGGATGGAAGAGGCTGGC
TCTGTTGCCCTGGAGGAACCTTGTGGAAAAAGAAAAGGACCGATTCTTCTCTGGTGTGGACTA
CATTGTAATTTTACAGATAACCTGTGGATCAGCCAAAGGAAGCCAGCAATCACTTATGGAACCC
GGGGGAACAGCTACTTCATGGTGGAGGTGAAATGCAGAGACCAGGATTTTCACTCAGGAACC
TTTGGTGGCATCCTTCATGAACCAATGGCTGATCTGGTTGCTCTTCTCGGTAGCCTGGTAGA
CTCGTCTGGTCATATCCTGGTCCCTGGAATCTATGATGAAGTGGTTCCTCTTACAGAAGAGG
AAATAAATACATACAAAGCCATCCATCTAGACCTAGAAGAATACCGGAATAGCAGCCGGGTT
GAGAAATTTCTGTTTCGATACTAAGGAGGAGATTCTAATGCACCTCTGGAGGTACCCATCTCT
TTCTATTTCATGGGATCGAGGGCGCGTTTGATGAGCCTGGAACCTAAAACAGTCATACCTGGCC
GAGTTATAGGAAAATTTTCAATCCGTCTAGTCCCTCACATGAATGTGTCTGCGGTGGAAAAA
CAGGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATAGTTCCAACAAGATGGTTGT
TTCCATGACTCTAGGACTACACCCGTGGATTGCAAATATTGATGACACCCAGTATCTCGCAG
CAAAAAGAGCGATCAGAACAGTGTGTTGGAACAGAACAGATATGATCCGGGATGGATCCACC
ATTCCAATTGCCAAAATGTTCCAGGAGATCGTCCACAAGAGCGTGGTGCTAATTCCGCTGGG
AGCTGTTGATGATGGAGAACATTCGCAGAATGAGAAAATCAACAGGTGGAACCTACATAGAGG
GAACCAAATTATTTGCTGCCTTTTTCTTAGAGATGGCCCAGCTCCAT**TAA**TCACAAGAACCT
TCTAGTCTGATCTGATCCACTGACAGATTACCTCCCCACATCCCTAGACAGGGATGGAAT
GTAAATATCCAGAGAATTTGGGTCTAGTATAGTACATTTTCCCTTCCATTTAAAATGTCTTG
GGATATCTGGATCAGTAATAAAATATTTCAAAGGCACAGATGTTGGAAATGGTTTAAAGGTCC
CCCACTGCACACCTTCCCTCAAGTCATAGCTGCTTGCAGCAACTTGATTTCCCAAGTCCTGT
GCAATAGCCCCAGGATTGGATTCCCTTCCAACCTTTTAGCATATCTCCAACCTTGCAATTTGA
TTGGCATAATCACTCCGGTTTGGCTTTCTAGGTCCTCAAGTGCTCGTGACACATAATCATTCC
ATCCAATGATCGCCTTTGCTTTACCACTCTTTCCCTTTTATCTTATTAATAAAAATGTTGGTC
TCCACCACTGNCTCCCAA
AAAAAAAAAA

103640-42204

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGSDPTK
GTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCT**ATG**GGACCTGTGCGGTT
GGGAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCCGAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAAGTGAAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCCTAGTGCAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCCACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAGGAGATCACAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCCAAAGTTGACCGAGAAGATCTT**TGA**ACCCTTGCTTTGAG
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACTCTATCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAE LSRTGRSREVL
ELGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK
GLVQKGVKVDLGIPLELWDEPSVEV TYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPA AETACLQETWTGKEITDGE EKTEGEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

[illegible]

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCTT
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG
T TACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCTCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAATG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGAT**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAAAATCATCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFPYELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK
KGKIQQQEELSAYQAPSPPAHSGFHYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

403360324

FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACTATGAGAGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAATATAAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCTCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCATTTTACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAAG
ACCTTGTAACAATAAATAATTCTTGTTAAGTTAAATCATTTTTGTCCTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

1094160-13304

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCCTGCTGCTGCTG
CTCCTGGCGGGAGCCCCCGCCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC
AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC
ACATGGA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEYF
IPVTTVLPDRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAAGCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA
GCCGCCAGTCCCGGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCCTGTTTTTAC
TCCTCCTTTTTCATTTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGGAAGAATGCGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTTTGTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTCAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAC
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT
CCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAAT
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAACACTTC
TAATTCTGTGATTAAATTTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISP EEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 37

GTTGCTCCGGCGGCGCTCGGGGAGGGAGCCAGCAGCCTAGGGCCTAGGCCCGGGCCACC**ATG**
GCGCTGCCTCCAGGCCCAGCCGCCCTCCGGCACACACTGCTGCTCCTGCCAGCCCTTCTGAG
CTCAGGTTGGGGGAGTTGGAGCCACAAATAGATGGTCAGACCTGGGCTGAGCGGGCACTTC
GGGAGAATGAACGCCACGCCTTCACCTGCCGGGTGGCAGGGGGCCTGGCACCCCCAGATTG
GCCTGGTATCTGGATGGACAGCTGCAGGAGGCCAGCACCTCAAGACTGCTGAGCGTGGGAGG
GGAGGCCTTCTCTGGAGGCACCAGCACCTTCACTGTCACTGCCCATCGGGCCCAGCATGAGC
TCAACTGCTCTCTGCAGGACCCCAGAAGTGGCCGATCAGCCAACGCCTCTGTCATCCTTAAT
GTGCAATTCAAGCCAGAGATTGCCCAAGTCGGCGCCAAGTACCAGGAAGCTCAGGGCCCAGG
CCTCCTGGTTGTCCTGTTTGCCCTGGTGCGTGCCAACCCGCCGGCCAATGTCACCTGGATCG
ACCAGGATGGGCCAGTGACTGTCAACACCTCTGACTTCCTGGTGCTGGATGCGCAGAACTAC
CCCTGGCTCACCAACCACACGGTGCAGCTGCAGCTCCGCAGCCTGGCACACAACCTCTCGGT
GGTGGCCACCAATGACGTGGGTGTCAACAGTGCGTCGCTTCCAGCCCCAGGCCCTCCCGGC
ACCCATCTCTGATATCAAGTGACTCCAACAACCTAAAACCTCAACAACGTGCGCCTGCCACGG
GAGAACATGTCCCTCCCGTCCAACCTTCAGCTCAATGACCTCACTCCAGATTCCAGAGCAGT
GAAACCAGCAGACCGGCAGATGGCTCAGAACACAGCCGGCCAGAGCTTCTGGACCCGGAGC
CCGGCGGCCTCCTCACCAGCCAAGGTTTCATCCGCCTCCAGTGCTGGGCTATATCTATCGA
GTGTCCAGCGTGAGCAGTGATGAGATCTGGCTCT**TGAG**CCCGAGGGCGAGACAGGAGTATTCTC
TTGGCCTCTGGACACCCTCCCATTCTCCTCAAGGCATCCTCTACCTAGCTAGGTCACCAACGT
GAAGAAGTTATGCCACTGCCACTTTTGCTTGCCCTCCTGGCTGGGGTGCCCTCCATGTCATG
CACGTGATGCATTTCACTGGGCTGTAACCCGCAGGGGCACAGGTATCTTTGGCAAGGCTACC
AGTTGGACGTAAGCCCCCTCATGCTGACTCAGGGTGGGCCCTGCATGTGATGACTGGGCCCTT
CCAGAGGGAGCTCTTTGGCCAGGGGTGTTGAGATGTCATCCAGCATCCAAGTGTTGGCATGGC
CTGCTGTATACCCACCCACAGTACTCCACAGCACCTTGTACAGTAGGCATGGGGCGTGCCT
GTGTGGGGGACAGGGAGGGCCCTGCATGGATTTTCTCCTCCTTCTATGCTATGTAGCCTTGTT
CCCTCAGGTAATAATTTAGGACCCTGCTAGCTGTGCAGAACCCAATTGCCCTTTGCACAGAAA
CCAACCCCTGACCCAGCGGTACCGGCCAAGCACAAACGTCTTTTGGCTGCACACGTCTCTG
CCCTTCACTTCTTCTCTTCTGTCCCCACCTCCTCTTGGGAATTCTAGGTTACACGTTGGACC
TTCTCTACTACTTCACTGGGCACTAGACTTTTCTATTGGCCTGTGCCATCGCCAGTATTAG
CACAAGTTAGGGAGGAAGAGGCAGGCGATGAGTCTAGTAGCACCCAGGACGGCTTGAGCTA
TGCATCATTTTCCTACGGCGTTAGCACTTTAAGCACATCCCCTAGGGGAGGGGTGAGTGAG
GGGCCCAGAGCCCTCTTTGTGGCTTCCCCACGTTTGGCCTTCTGGGATTCACTGTGAGTGTC
CTGAGCTCTCGGGGTGATGGTTTTTCTCTCAGCATGTCTCCTCCACCACGGGACCCAGCC
CTGACCAACCCATGGTTGCCTCATCAGCAGGAAGGTGCCCTTCTGGAGGATGGTCGCCACA
GGCACATAATTCAACAGTGTGGAAGCTTTAGGGGAACATGGAGAAAGAAGGAGACCACATAC
CCCAAAGTGACCTAAGAACACTTTAAAAAGCAACATGTAAATGATTGGAAATTAATATAGTA
CAGAATATATTTTTCCCTTGTTGAGATCTTCTTTTGTAAATGTTTTTCATGTTACTGCCTAGG
GCGGTGCTGAGCACACAGCAAGTTTAATAAACTTGACTGAATTCATTTAAAAAAAAAAAAAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQGPVTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGC
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCG
GCTCGGAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPFVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRGCGQAVRLTHVLTGKNLHTHHFPSPL
SNNQEVSAFGEDEGDDLDLWTVRCGQHWEREAAVRFQHVGTSVFELSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

Downloaded from www.nrjonline.com

FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACCTCATCTTCTTTGGATGAGATGAACACTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAAGTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAACCAAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

.><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCCTCGCC**ATG**AAAG
CCCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**
ACTCATTCCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCACCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAA

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCCTCGCC**ATG**AAAG

><subunit 1 of 1, 125 aa, 1 stop

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN

Important features of the protein:

amino acids 1-18

amino acids 77-81, 88-92

amino acids 84-90

amino acids 85-98

FIGURE 45

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCA
GTCGGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**AT**
GGCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTC
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCCGTAAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA
TGGAGGCTCGGGCAGCTATTCCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAG
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTTGTATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA
TATTGCAGTTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC
CTGTGATGCCCTAAGAAGCATTAAAGATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGQLKESGKQHGFASFSDYYYKWSSADSCNMSGELITIVVLLGIA
FVVYKLFSLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPYPPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318